

IN THE CLAIMS

Claims 4 and 6-10 have been amended as follows:

4 (Amended). A synthetic peptide according to any one of claim 1, selected from:

(i) peptides **pep1**, **pep2**, and **pep3** of the sequences:

(**pep1**) Ile-Val-Leu

(**pep2**) Glu-Phe-Leu-Asn-Arg-Trp-Ile-Thr (SEQ ID NO:1)

(**pep3**) Arg-Met-Leu-Thr (SEQ ID NO:2)

a2 (ii) peptides obtained from **pep2** by deletion of one or more amino acid residues;

(iii) peptides obtained by addition to peptides (i) or (ii) of one or more natural or non-natural amino acid residues;

(iv) peptides obtained by replacement of one or more amino acid residues of peptides (i) to (iii) by the corresponding D-stereomer, by another natural amino acid residue or by a non-natural amino acid residue;

(v) chemical derivatives of the peptides (i) to (iv);

(vi) cyclic derivatives of peptides (i) to (v);

(vii) dual peptides consisting of two of the same or different peptides (i) to (vi), wherein the peptides are covalently linked to one another directly or through a spacer; and

(viii) multimers comprising a number of the same or different peptides (i) to (vi).

a3 Sub B1 6 (Amended). A synthetic peptide according to claim 5, selected from:

(**pep1**) Ile-Val-Leu
(**pep4**) Asn-Ile-Asn-Val-Ile-Val-Leu (SEQ ID NO:3),
(**pep5**) Ile-Val-Leu-Glu-Leu-Lys-Gly (SEQ ID NO:4),
(**pep6**) Asn-Val-Ile-Val-Leu (SEQ ID NO:5)
(**pep7**) Ala-Val-Leu
(**pep8**) Ile-Ala-Leu
(**pep9**) Ile-Val-Ala
(**pep10**) Glu-Val-Leu

(**pep11**, linear) and (**pep12**, cyclic) Cys-Ile-Val-Leu-Ala-Cys (SEQ ID NO:6) and,

(**pep13**, linear) and (**pep14**, cyclic) Cys-Ile-Val-Leu-Ala-Ala-Cys (SEQ ID NO:7).

Sub B1 3 (Amended). The synthetic peptide Glu-Phe-Leu-Asn-Arg-Trp-Ile-Thr (SEQ ID NO:1) (**pep2**), and derivatives thereof according to claim 4, obtained by:

(a) elongation by up to 4 further amino acid residues at the C and/or N terminal ends, preferably according to the natural sequence of IL-2;

a³ cont (b) substitution of the Glu residue by a natural or non-natural charged or polar charged amino acid residue, preferably selected from Lys, Arg, Asp, Gln, Asn;

(c) substitution of the Phe residue by a natural or non-natural hydrophobic aliphatic or aromatic amino acid residue, preferably selected from Ala, Val, Ile, Leu, Tyr, Trp, Phe, Met, Nle;

(d) substitution of the Leu residue by a natural or non-natural hydrophobic aliphatic or aromatic amino acid

residue, preferably selected from Ala, Val, Ile, Leu, Tyr, Trp, Phe, Met, Nle;

(e) substitution of the important Asn residue by a hydrophilic, non-charged, aliphatic natural or non-natural amino acid residue such as Gln;

(f) substitution of the Arg residue by a positively charged, natural or non-natural amino acid residue, preferably selected from Lys, Orn, homoArg;

(g) substitution of the Trp residue by a natural or non-natural hydrophobic, aliphatic or aromatic, amino acid residue, preferably selected from Tyr, Ile, Leu, Nle, Tic, Phe, 4-phenyl-Phe, 4-methyl-Phe;

sw B1
(h) substitution of the Ile residue by a natural or non-natural hydrophobic, aliphatic or aromatic, amino acid residue, preferably selected from Tyr, Phe, Leu, Nle, Tic;

Q3 Cont
(i) substitution of the Thr residue by an aliphatic hydrophobic amino acid residue such as Ala, Ile, Leu, or a hydroxy- or thio-containing amino acid residue preferably selected from Cys, Ser;

(j) truncation by up to 4 amino acid residues from either the C or N terminal;

(k) amidation of the C-terminal Thr;

(l) cyclization of pep2 or of any peptide of (a) to (k); and

(m) any combination of (a) to (l).

8 (Amended). A peptide according to claim 7, selected from:

(pep2) Glu-Phe-Leu-Asn-Arg-Trp-Ile-Thr (SEQ ID NO:1)

(pep15) Ile-Val-Glu-Phe-Leu-Asn-Arg-Trp-Ile-Thr (SEQ ID NO:8)

(pep16) Glu-Phe-Leu-Asn-Arg-Trp-Ile-Thr-Phe-Cys (SEQ ID NO:9)

(pep17) Ala-Thr-Ile-Val-Glu-Phe-Leu-Asn-Arg-Trp-Ile-Thr (SEQ ID NO:10)

(pep18) Glu-Phe-Leu-Asn-Arg-Trp-Ile-Thr-Phe-Cys-Gln-Ser (SEQ ID NO:11)

(pep19) Leu-Asn-Arg-Trp-Ile-Thr (SEQ ID NO:12)

(pep20) Arg-Trp-Ile-Thr (SEQ ID NO:13)

(pep21) Glu-Phe-Leu-Asn (SEQ ID NO:14)

(pep22) Ala-Phe-Leu-Asn-Arg-Trp-Ile-Thr (SEQ ID NO:15)

(pep23) Lys-Phe-Leu-Asn-Arg-Trp-Ile-Thr (SEQ ID NO:16)

(pep24) Glu-Ala-Leu-Asn-Arg-Trp-Ile-Thr (SEQ ID NO:17)

(pep25) Glu-Val-Leu-Asn-Arg-Trp-Ile-Thr (SEQ ID NO:18)

(pep26) Glu-Phe-Ala-Asn-Arg-Trp-Ile-Thr (SEQ ID NO:19)

(pep27) Glu-Phe-Leu-Ala-Arg-Trp-Ile-Thr (SEQ ID NO:20)

(pep28) Glu-Phe-Leu-Asn-Ala-Trp-Ile-Thr (SEQ ID NO:21)

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a3
cont.

(~~pep29~~) Glu-Phe-Leu-Asn-Glu-Trp-Ile-Thr (SEQ ID
NO:22)

(~~pep30~~) Glu-Phe-Leu-Asn-Arg-Ala-Ile-Thr (SEQ ID
NO:23)

(~~pep31~~) Glu-Phe-Leu-Asn-Arg-Trp-Ala-Thr (SEQ ID
NO:24)

(~~pep32~~) Glu-Phe-Leu-Asn-Arg-Trp-Ile-Ala (SEQ ID
NO:25)

(~~pep33~~) Glu-Phe-Leu-Asn-Arg-Trp-Ile-Thr-NH₂ (SEQ ID
NO:26) and,

(~~pep34~~, linear) and (~~pep35~~, cyclic) Cys-Glu-Phe-
Leu-Asn-Arg-Trp-Ile-Thr-Ala-Cys (SEQ ID NO:27).

9 (Amended). The synthetic peptide Arg-Met-Leu-Thr
(SEQ ID NO:2) (~~pep3~~), and derivatives thereof according to
claim 4, obtained by:

(a) elongation by up to 4 further amino acid
residues at the C and/or N terminal end, preferably according
to the natural sequence of IL-2;

(b) substitution of the Arg residue by a natural or
non-natural positively charged amino acid residue, preferably
selected from Lys, Orn, homoArg, diaminobutyric acid;

(c) substitution of the Met residue by a natural or
non-natural hydrophobic, aliphatic or aromatic, amino acid
residue, preferably selected from Phe, Tyr, Ile, Leu, Nle,
Tic;

(d) substitution of the Leu residue by a natural or
non-natural hydrophobic, aliphatic or aromatic, amino acid
residue, preferably selected from Phe, Tyr, Nle, Tic;

(e) substitution of the Thr residue by an aliphatic hydrophobic amino acid residue such as Ala, Ile, Leu, or a hydroxy- or thio-containing amino acid residue such as Ser, Cys;

(f) amidation of the C-terminal Thr residue;

(g) cyclization of pep3 or of any peptide of (a) to (f); and

(h) any combination of (a) to (g).

10 (Amended). A peptide according to claim 9, selected from:

(pep3) Arg-Met-Leu-Thr (SEQ ID NO:2)
(pep36) Ala-Met-Leu-Thr (SEQ ID NO:28)
(pep37) Arg-Ala-Leu-Thr (SEQ ID NO:29)
(pep38) Arg-Met-Ala-Thr (SEQ ID NO:30)
(pep39) Arg-Met-Leu-Ala (SEQ ID NO:31)
(pep40) Lys-Met-Leu-Thr (SEQ ID NO:32)
(pep41) Arg-Val-Leu-Thr (SEQ ID NO:33)
(pep42) Arg-Met-Leu-Thr-NH₂ (SEQ ID NO:34)
(pep43) Pro-Lys-Leu-Thr-Arg-Met-Leu-Thr (SEQ ID

NO:35)

(pep44) Arg-Met-Leu-Thr-Phe-Lys-Phe-Tyr (SEQ ID NO:36) and,

(pep45, linear) and (pep46, cyclic) Cys-Arg-Met-Leu-Thr-Ala-Cys (SEQ ID NO:37).